What is claimed is:

1. A transgenic plant comprising a recombinant polynucleotide encoding a polypeptide having a HAP3 subfamily B domain,

wherein said polypeptide has the property of SEQ ID NO: 4 of regulating abiotic stress tolerance in a plant when said polypeptide is overexpressed, and wherein:

the HAP3 subfamily B domain is sufficiently homologous to the B domain of SEQ ID NO: 4 that the polypeptide binds to a transcription regulating region comprising the motif CCAAT; and

wherein said binding confers increased abiotic stress tolerance in said transgenic plant as compared to a non-transformed plant that does not overexpress the polypeptide.

2. The transgenic plant of Claim 1, wherein the HAP3 subfamily B domain is at least 83% identical in amino acid sequence to the B domain of SEQ ID NO: 4, and wherein said HAP3 subfamily B domain comprises:

Asn-$(Xaa)_4$-Lys-$(Xaa)_{33-34}$-Asn-Gly;

where Xaa is any amino acid residue;

and overexpression of said polypeptide confers increased abiotic stress tolerance in said transgenic plant as compared to a non-transformed plant that does not overexpress the polypeptide.

3. The transgenic plant of Claim 2, wherein said HAP3 subfamily B domain comprises:

Ser-$(Xaa)_9$-Asn-$(Xaa)_4$-Lys-$(Xaa)_{33-34}$-Asn-Gly;

where Xaa is any amino acid residue;

and overexpression of said polypeptide confers increased abiotic stress tolerance in said transgenic plant as compared to a non-transformed plant that does not overexpress the polypeptide.

4. The transgenic plant of Claim 1, wherein said polypeptide comprises SEQ ID NO: 4.

5. The transgenic plant of Claim 1, wherein said recombinant polynucleotide has a nucleotide sequence that hybridizes over its full length to the complement of SEQ ID NO:3 under stringent conditions including two wash steps of 6x SSC and 65° C for 10-30 minutes.

6. The transgenic plant of Claim 5, wherein said nucleotide sequence comprises SEQ ID NO: 3.

7. The transgenic plant of Claim 1, wherein said abiotic stress tolerance is selected from the group consisting of heat tolerance, drought stress and salt stress.

8. The transgenic plant of Claim 1, wherein said transgenic plant is characterized by altered sugar sensing as compared to a non-transformed plant that does not overexpress the recombinant polynucleotide.

9. The transgenic plant of Claim 1, wherein the plant is selected from the group consisting of: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, clover, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach, squash, sweet corn, tobacco, tomato, watermelon, mint and other labiates, fruit trees, rosaceous fruits, citrus, and brassicas.

10. The transgenic plant of Claim 1, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to said recombinant polynucleotide.

11. The transgenic plant of Claim 1, wherein said HAP3 subfamily B domain is at least 83% identical with the B domain of SEQ ID NO: 4.

12. A method for producing a transgenic plant having increased tolerance to osmotic stress, the method steps comprising:

(a) providing an expression vector comprising

(i) a nucleotide sequence that encodes a polypeptide having a B domain that is sufficiently homologous to the B domain of SEQ ID NO: 3 that the polypeptide binds to a transcription regulating region comprising the motif CCAAT and has the property of regulating abiotic stress tolerance in a plant as compared to a non-transformed plant that does not overexpress the polypeptide;

wherein said nucleotide sequence comprises a B domain that is at least 83% identical with the B domain of SEQ ID NO: 4; and

(ii) regulatory elements flanking the nucleotide sequence, said regulatory elements being effective to control expression of said nucleotide sequence in a target plant;

(b) introducing the expression vector into a plant cell;

(c) growing the plant cell into a plant and allowing the plant to overexpress said polypeptide; and;

(d) identifying one or more abiotic stress tolerant plants so produced with increased abiotic stress tolerance by comparing said one or more abiotic stress tolerant plants with one or more non-transformed plants that do not overexpress the polypeptide.

13. The method of Claim 12, wherein said nucleotide sequence hybridizes over its full length to the complement of SEQ ID NO: 3 under stringent conditions including two wash steps of 6x SSC and 65° C for 10-30 minutes.

14. The method of Claim 12, wherein said abiotic stress tolerance is selected from the group consisting of heat tolerance, drought stress and salt stress.

15. The method of Claim 12, the method steps further comprising:

(e) crossing one of said abiotic stress tolerant plants with itself or another plant;

(f) selecting seed that develops as a result of said crossing; and growing a progeny plant from the seed, thus producing a transgenic progeny plant having increased tolerance to abiotic stress.

16. The method of Claim 15, wherein:

said progeny plant expresses mRNA that encodes a DNA-binding protein that binds to a CCAAT DNA regulatory sequence and induces expression of a plant trait gene; and

said mRNA is expressed at a level greater than a non-transformed plant that does not overexpress said DNA-binding protein.

17. A method for increasing a plant's tolerance to abiotic stress, said method comprising:

(a) providing a vector comprising:

regulatory elements flanking the polynucleotide sequence, said regulatory elements being effective to control expression of said polynucleotide sequence in a target plant; and

a polynucleotide sequence that encodes a polypeptide having a B domain sufficiently homologous to the B domain of SEQ ID NO: 3 that the polypeptide binds to a transcription regulating region comprising the motif CCAAT and has the property of SEQ ID NO:4 of regulating abiotic stress tolerance in a plant, wherein said binding confers increased abiotic stress tolerance in said transgenic plant as compared to a non-transformed plant that does not overexpress the polypeptide; and

(b) transforming the target plant with said vector to generate a transformed plant with increased tolerance to osmotic stress.

18. The method of Claim 17, wherein said polynucleotide comprises:

(i) SEQ ID NO: 3;

(ii) a nucleotide sequence that encodes SEQ ID NO: 4;

(iii) a nucleotide sequence that hybridizes to the nucleotide sequence of (i) or (ii) under stringent conditions including two wash steps of 6x SSC and 65° C for 10-30 minutes; or

(iv) a nucleotide sequence encoding a polypeptide that comprises a B domain that is at least 83% identical with the B domain of SEQ ID NO: 4.

19. The method of Claim 17, wherein said abiotic stress tolerance is selected from the group consisting of heat tolerance, cold germination, drought stress and salt stress.

20. A recombinant polynucleotide comprising a nucleotide sequence at least 99.6% identical to SEQ ID NO: 3.

21. The recombinant polynucleotide of Claim 20, wherein said recombinant polynucleotide comprises SEQ ID NO: 3.

22. The recombinant polynucleotide of Claim 20, wherein said recombinant polynucleotide is incorporated into an expression vector comprising one or more regulatory elements that are effective to control expression of said recombinant polynucleotide in a target plant

23. The recombinant polynucleotide of Claim 22, wherein said recombinant polynucleotide is incorporated into a cultured host cell.